

1
SEQUENCE LISTING

<110> Valladeau, Jenny
 Ravel, Odile
 Bates, Elizabeth Ester Mary
 Ford, John
 Lebecque, Serge J.E.
 Saeland, Sem

<120> Isolated Mammalian Membrane Protein Genes; Related Reagents

<130> SF0695 B

<140> US 09/862,802
 <141> 2001-05-22

<150> US 60/053,080
 <151> 1997-07-09

<150> US 09/111,470
 <151> 1998-07-08

<160> 13

<170> PatentIn version 3.1

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 ctccactagt tgagtgaag gaaggaggta atttaccacc atgttttggtt cctgtttata 180
 agatgtttta agaaagattt gaaacagatt ttctgaagaa agcagaagct ctcttcccat 240
 t atg act tcg gaa atc act tat gct gaa gtg agg ttc aaa aat gaa ttc 289
 Met Thr Ser Glu Ile Thr Tyr Ala Glu Val Arg Phe Lys Asn Glu Phe
 1 5 10 15
 aag tcc tca ggc atc aac aca gcc tct tct gca gct tcc aag gag agg 337
 Lys Ser Ser Gly Ile Asn Thr Ala Ser Ser Ala Ala Ser Lys Glu Arg
 20 25 30
 act gcc cct ctc aaa agt aat acc gga ttc ccc aag ctg ctt tgt gcc 385
 Thr Ala Pro Leu Lys Ser Asn Thr Gly Phe Pro Lys Leu Leu Cys Ala
 35 40 45

tca ctg ttg ata ttt ttc ctg cta ttg gca atc tca ttc ttt att gct Ser Leu Leu Ile Phe Phe Leu Leu Leu Ala Ile Ser Phe Phe Ile Ala 50 55 60	433
ttt gtc att ttc ttt caa aaa tat tct cag ctt ctt gaa aaa aag act Phe Val Ile Phe Phe Gln Lys Tyr Ser Gln Leu Leu Glu Lys Lys Thr 65 70 75 80	481
aca aaa gag ctg gtt cat aca aca ttg gag tgt gtg aaa aaa aat atg Thr Lys Glu Leu Val His Thr Thr Leu Glu Cys Val Lys Lys Asn Met 85 90 95	529
ccc gtg gaa gag aca gcc tgg agc tgt tgc cca aag aat tgg aag tca Pro Val Glu Glu Thr Ala Trp Ser Cys Cys Pro Lys Asn Trp Lys Ser 100 105 110	577
ttt agt tcc aac tgc tac ttt att tct act gaa tca gca tct tgg caa Phe Ser Ser Asn Cys Tyr Phe Ile Ser Thr Glu Ser Ala Ser Trp Gln 115 120 125	625
gac agt gag aag gac tgt gct aga atg gag gct cac ctg ctg gtg ata Asp Ser Glu Lys Asp Cys Ala Arg Met Glu Ala His Leu Leu Val Ile 130 135 140	673
aac act caa gaa gag cag gat ttc atc ttc cag aat ctg caa gaa gaa Asn Thr Gln Glu Glu Gln Asp Phe Ile Phe Gln Asn Leu Gln Glu Glu 145 150 155 160	721
tct gct tat ttt gtg ggg ctc tca gat cca gaa ggt cag cga cat tgg Ser Ala Tyr Phe Val Gly Leu Ser Asp Pro Glu Gly Gln Arg His Trp 165 170 175	769
caa tgg gtt gat cag aca cca tac aat gaa agt tcc aca ttc tgg cat Gln Trp Val Asp Gln Thr Pro Tyr Asn Glu Ser Ser Thr Phe Trp His 180 185 190	817
cca cgt gag ccc agt gat ccc aat gag cgc tgc gtt gtg cta aat ttt Pro Arg Glu Pro Ser Asp Pro Asn Glu Arg Cys Val Val Leu Asn Phe 195 200 205	865
cgt aaa tca ccc aaa aga tgg ggc tgg aat gat gtt aat tgt ctt ggt Arg Lys Ser Pro Lys Arg Trp Gly Trp Asn Asp Val Asn Cys Leu Gly 210 215 220	913
cct caa agg tca gtt tgt gag atg atg aag atc cac tta tgaactgaac Pro Gln Arg Ser Val Cys Glu Met Met Lys Ile His Leu 225 230 235	962
attctccatg aacaggtggt tggattggta tctgtcattg tagggataga taataagctc	1022
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Thr Ala Pro Leu Lys Ser Asn Thr Gly Phe Pro Lys Leu Leu Cys Ala
 35 40 45

Ser Leu Leu Ile Phe Phe Leu Leu Leu Ala Ile Ser Phe Phe Ile Ala
 50 55 60

Phe Val Ile Phe Phe Gln Lys Tyr Ser Gln Leu Leu Glu Lys Lys Thr
 65 70 75 80

Thr Lys Glu Leu Val His Thr Thr Leu Glu Cys Val Lys Lys Asn Met
 85 90 95

Pro Val Glu Glu Thr Ala Trp Ser Cys Cys Pro Lys Asn Trp Lys Ser
 100 105 110

Phe Ser Ser Asn Cys Tyr Phe Ile Ser Thr Glu Ser Ala Ser Trp Gln
 115 120 125

Asp Ser Glu Lys Asp Cys Ala Arg Met Glu Ala His Leu Leu Val Ile
 130 135 140

Asn Thr Gln Glu Glu Gln Asp Phe Ile Phe Gln Asn Leu Gln Glu Glu
 145 150 155 160

Ser Ala Tyr Phe Val Gly Leu Ser Asp Pro Glu Gly Gln Arg His Trp
 165 170 175

Gln Trp Val Asp Gln Thr Pro Tyr Asn Glu Ser Ser Thr Phe Trp His
 180 185 190

Pro Arg Glu Pro Ser Asp Pro Asn Glu Arg Cys Val Val Leu Asn Phe
 195 200 205

Arg Lys Ser Pro Lys Arg Trp Gly Trp Asn Asp Val Asn Cys Leu Gly
 210 215 220

[illegible]

ctg ggc ctc ggc ctg ctg ctg ctg gtc atc atc tgt gtg gtt gga ttc Leu Gly Leu Gly Leu Leu Leu Leu Val Ile Ile Cys Val Val Gly Phe 45 50 55 60	436
caa aat tcc aaa ttt cag agg gac ctg gtg acc ctg aga aca gat ttt Gln Asn Ser Lys Phe Gln Arg Asp Leu Val Thr Leu Arg Thr Asp Phe 65 70 75	484
agc aac ttc acc tca aac act gtg gcg gag atc cag gca ctg act tcc Ser Asn Phe Thr Ser Asn Thr Val Ala Glu Ile Gln Ala Leu Thr Ser 80 85 90	532
cag ggc agc agc ttg gaa gaa acg ata gca tct ctg aaa gct gag gtg Gln Gly Ser Ser Leu Glu Glu Thr Ile Ala Ser Leu Lys Ala Glu Val 95 100 105	580
gag ggt ttc aag cag gaa cgg cag gca ggg gta tct gag ctc cag gaa Glu Gly Phe Lys Gln Glu Arg Gln Ala Gly Val Ser Glu Leu Gln Glu 110 115 120	628
cac act acg cag aag gca cac cta ggc cac tgt ccc cac tgc cca tct His Thr Thr Gln Lys Ala His Leu Gly His Cys Pro His Cys Pro Ser 125 130 135 140	676
gtg tgt gtc cca gtt cat tct gaa atg ctc ctg cga gtc cag cag ctg Val Cys Val Pro Val His Ser Glu Met Leu Leu Arg Val Gln Gln Leu 145 150 155	724
gtg caa gac ctg aag aaa ctg acc tgc cag gtg gct act ctc aac aac Val Gln Asp Leu Lys Lys Leu Thr Cys Gln Val Ala Thr Leu Asn Asn 160 165 170	772
aat gcc tcc act gaa ggg acc tgc tgc ccc gtc aac tgg gtg gag cac Asn Ala Ser Thr Glu Gly Thr Cys Cys Pro Val Asn Trp Val Glu His 175 180 185	820
caa gac agc tgc tac tgg ttc tct cac tct ggg atg tcc tgg gcc gag Gln Asp Ser Cys Tyr Trp Phe Ser His Ser Gly Met Ser Trp Ala Glu 190 195 200	868
gct gag aag tac tgc cag ctg aag aac gcc cac ctg gtg gtc atc aac Ala Glu Lys Tyr Cys Gln Leu Lys Asn Ala His Leu Val Val Ile Asn 205 210 215 220	916
tcc agg gag gag cag aat ttt gtc cag aaa tat cta ggc tcc gca tac Ser Arg Glu Glu Gln Asn Phe Val Gln Lys Tyr Leu Gly Ser Ala Tyr 225 230 235	964
acc tgg atg ggc ctc agt gac cct gaa gga gcc tgg aag tgg gtg gat Thr Trp Met Gly Leu Ser Asp Pro Glu Gly Ala Trp Lys Trp Val Asp 240 245 250	1012
gga aca gac tat gcg acc ggc ttc cag aac tgg aag cca ggc cag cca Gly Thr Asp Tyr Ala Thr Gly Phe Gln Asn Trp Lys Pro Gly Gln Pro 255 260 265	1060
gac gac tgg cag ggg cac ggg ctg ggt gga ggc gag gac tgt gct cac Asp Asp Trp Gln Gly His Gly Leu Gly Gly Gly Glu Asp Cys Ala His 270 275 280	1108


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ttc cat cca gac ggc agg tgg aat gac gac gtc tgc cag agg ccc tac      1156
Phe His Pro Asp Gly Arg Trp Asn Asp Asp Val Cys Gln Arg Pro Tyr
285                      290                      295                      300

cac tgg gtc tgc gag gct ggc ctg ggt cag acc agc cag gag agt cac      1204
His Trp Val Cys Glu Ala Gly Leu Gly Gln Thr Ser Gln Glu Ser His
305                      310                      315

tgagctgcct ttggtgggac caccgggcca cagaaatggc ggtgggagga ggactcttct      1264
cacgacctcc tcgcaagacc gctctgggag agaaataagc actgggagat tggaagcact      1324
gctaacattt tgaatttttt tctctttaat tttaaaaaga tggatatagtg ttcttaagct      1384
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<222> (608)..(673)
<223> short form lacks nucleotides 608-673

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<220>
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<223> ASGPRm (Table 2) has sequence insert encoding GEE between nucleot
ides 775-776

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<222> (1064)..(1064)
<223> nucleotide 1064 of DCMP2s may be A, which would encode Asn rather
than Asp at the residue numbered 270

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Met Thr Arg Thr Tyr Glu Asn Phe Gln Tyr Leu Glu Asn Lys Val Lys
1                      5                      10                      15

```

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Val Gln Gly Phe Lys Asn Gly Pro Leu Pro Leu Gln Ser Leu Leu Gln
20                      25                      30

```

```

Arg Leu Arg Ser Gly Pro Cys His Leu Leu Leu Ser Leu Gly Leu Gly
35                      40                      45

```

```

Leu Leu Leu Leu Val Ile Ile Cys Val Val Gly Phe Gln Asn Ser Lys

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50

55

60

Phe Gln Arg Asp Leu Val Thr Leu Arg Thr Asp Phe Ser Asn Phe Thr
65 70 75 80

Ser Asn Thr Val Ala Glu Ile Gln Ala Leu Thr Ser Gln Gly Ser Ser
85 90 95

Leu Glu Glu Thr Ile Ala Ser Leu Lys Ala Glu Val Glu Gly Phe Lys
100 105 110

Gln Glu Arg Gln Ala Gly Val Ser Glu Leu Gln Glu His Thr Thr Gln
115 120 125

Lys Ala His Leu Gly His Cys Pro His Cys Pro Ser Val Cys Val Pro
130 135 140

Val His Ser Glu Met Leu Leu Arg Val Gln Gln Leu Val Gln Asp Leu
145 150 155 160

Lys Lys Leu Thr Cys Gln Val Ala Thr Leu Asn Asn Asn Ala Ser Thr
165 170 175

Glu Gly Thr Cys Cys Pro Val Asn Trp Val Glu His Gln Asp Ser Cys
180 185 190

Tyr Trp Phe Ser His Ser Gly Met Ser Trp Ala Glu Ala Glu Lys Tyr
195 200 205

Cys Gln Leu Lys Asn Ala His Leu Val Val Ile Asn Ser Arg Glu Glu
210 215 220

Gln Asn Phe Val Gln Lys Tyr Leu Gly Ser Ala Tyr Thr Trp Met Gly
225 230 235 240

Leu Ser Asp Pro Glu Gly Ala Trp Lys Trp Val Asp Gly Thr Asp Tyr
245 250 255

Ala Thr Gly Phe Gln Asn Trp Lys Pro Gly Gln Pro Asp Asp Trp Gln
260 265 270

Gly His Gly Leu Gly Gly Gly Glu Asp Cys Ala His Phe His Pro Asp
275 280 285

Gly Arg Trp Asn Asp Asp Val Cys Gln Arg Pro Tyr His Trp Val Cys

290

295

300

Glu Ala Gly Leu Gly Gln Thr Ser Gln Glu Ser His
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Asp His His Gln Leu Arg Lys Gly Pro Pro Pro Pro Gln Pro Leu Leu
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Gln Arg Leu Cys Ser Gly Pro Arg Leu Leu Leu Leu Ser Leu Gly Leu
 35 40 45

Ser Leu Leu Leu Leu Val Val Val Cys Val Ile Gly Ser Gln Asn Ser
 50 55 60

Gln Leu Gln Glu Glu Leu Arg Gly Leu Arg Glu Thr Phe Ser Asn Phe
 65 70 75 80

Thr Ala Ser Thr Glu Ala Gln Val Lys Gly Leu Ser Thr Gln Gly Gly
 85 90 95

Asn Val Gly Arg Lys Met Lys Ser Leu Glu Ser Gln Leu Glu Lys Gln
 100 105 110

Gln Lys Asp Leu Ser Glu Asp His Ser Ser Leu Leu Leu His Val Lys
 115 120 125

Gln Phe Val Ser Asp Leu Arg Ser Leu Ser Cys Gln Met Ala Ala Leu
 130 135 140

Gln Gly Asn Gly Ser Glu Arg Thr Cys Cys Pro Val Asn Trp Val Glu
 145 150 155 160

His Glu Arg Ser Cys Tyr Trp Phe Ser Arg Ser Gly Lys Ala Trp Ala
 165 170 175

Asp Ala Asp Asn Tyr Cys Arg Leu Glu Asp Ala His Leu Val Val Val
 180 185 190

Thr Ser Trp Glu Glu Gln Lys Phe Val Gln His His Ile Gly Pro Val
 195 200 205

Asn Thr Trp Met Gly Leu His Asp Gln Asn Gly Pro Trp Lys Trp Val
 210 215 220

Asp Gly Thr Asp Tyr Glu Thr Gly Phe Lys Asn Trp Arg Pro Glu Gln
 225 230 235 240

Pro Asp Asp Trp Tyr Gly His Gly Leu Gly Gly Gly Glu Asp Cys Ala
 245 250 255

His Phe Thr Asp Asp Gly Arg Trp Asn Asp Asp Val Cys Gln Arg Pro
 260 265 270

Tyr Arg Trp Val Cys Glu Thr Glu Leu Asp Lys Ala Ser Gln Glu Pro
 275 280 285

Pro Leu Leu
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 <213> Unknown

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 1 5 10 15

Asp His Pro Phe His Gln Gly Pro Pro Pro Ala Gln Pro Leu Ala Gln
 20 25 30

Arg Leu Cys Ser Met Val Cys Phe Ser Leu Leu Ala Leu Ser Phe Asn
 35 40 45

Ile Leu Leu Leu Val Val Ile Cys Val Thr Gly Ser Gln Ser Ala Gln
 50 55 60

Leu Gln Ala Glu Leu Arg Ser Leu Lys Glu Ala Phe Ser Asn Phe Ser

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 <223> protein coding sequence

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 t a t t t t c t t a t g t t a a g a g g t t g c a t t t c c c t t a t c t c g c c c t g g t g a t t c t a t g c t g t g 120
 g t t t c t t g t t c t c a t c t c g t t t a t c c t a g t g a g a c a t g t c t c t t c t t t c a t a c a a c t g t g 180
 c a a t a t g a c a a c t t a t c a c a g t g a t t g g t t c t c a t a t a c t a t a g a g c c t t a g a g a a g g a a 240
 c a a g g c t c t c t t c t g a c g g a g g a a g a t t t t t t c t t g a t a t g g c t c a g a a t c a c t 296
 Met Ala Ser Glu Ile Thr
 1 5
 t a t g c a g a a g t g a a g t t c a a g a a t g a a t c c a a c t c c t t g c a c a c c t a c 344
 Tyr Ala Glu Val Lys Phe Lys Asn Glu Ser Asn Ser Leu His Thr Tyr
 10 15 20
 t c a g a a t c t c c t g c a g c t c c c a g a g a g a a a c c t a t c c g t g a t c t a a g a 392
 Ser Glu Ser Pro Ala Ala Pro Arg Glu Lys Pro Ile Arg Asp Leu Arg
 25 30 35
 a a g c c t g g t t c c c c c t c a c t g c t t c t t a c a t c c c t g a t g c t a c t t c t c 440
 Lys Pro Gly Ser Pro Ser Leu Leu Leu Thr Ser Leu Met Leu Leu Leu
 40 45 50
 c t g c t g c t g g c a a t c a c a t t c t t a g t t g c t t t t a t c a t t t a t t t t c a a 488
 Leu Leu Leu Ala Ile Thr Phe Leu Val Ala Phe Ile Ile Tyr Phe Gln
 55 60 65 70
 a a g t a c t c t c a a c t t g a a g a a a a a g c t g c a a a a a t a t a a t g 536
 Lys Tyr Ser Gln Leu Leu Glu Glu Lys Lys Ala Ala Lys Asn Ile Met
 75 80 85
 c a c a a t g a a t t g a a c t g c a c a a a a g t g t t t c a c c c a t g g a a g a c a a a 584
 His Asn Glu Leu Asn Cys Thr Lys Ser Val Ser Pro Met Glu Asp Lys
 90 95 100
 g t c t g g a g c t g t t g c c c a a a g a t t g g a g g c t a t t t g g t t c c c a c t g c 632
 Val Trp Ser Cys Cys Pro Lys Asp Trp Arg Leu Phe Gly Ser His Cys
 105 110 115
 t a c t t g g t t c c c a c a g t t t c t t c a t c a g c a t c t t g g a a c a a g a g t g a g 680
 Tyr Leu Val Pro Thr Val Ser Ser Ser Ala Ser Trp Asn Lys Ser Glu
 120 125 130

12

gag aac tgc tcc cgc atg ggt gct cat cta gtg gtg atc caa agc cag	728
Glu Asn Cys Ser Arg Met Gly Ala His Leu Val Val Ile Gln Ser Gln	
135 140 145 150	
gaa gag cag gat ttc atc act ggg atc ttg gac act cat gct gct tat	776
Glu Glu Gln Asp Phe Ile Thr Gly Ile Leu Asp Thr His Ala Ala Tyr	
155 160 165	
ttt ata ggg ttg tgg gat aca ggc cat cgg caa tgg caa tgg gtt gat	824
Phe Ile Gly Leu Trp Asp Thr Gly His Arg Gln Trp Gln Trp Val Asp	
170 175 180	
cag aca cca tat gaa gaa agt atc aca ttc tgg cac aat ggt gag ccc	872
Gln Thr Pro Tyr Glu Glu Ser Ile Thr Phe Trp His Asn Gly Glu Pro	
185 190 195	
agc agt ggc aat gaa aaa tgt gct aca ata att tac cgt tgg aag act	920
Ser Ser Gly Asn Glu Lys Cys Ala Thr Ile Ile Tyr Arg Trp Lys Thr	
200 205 210	
gga tgg ggc tgg aac gat atc tct tgc agt ctt aaa cag aag tca gtt	968
Gly Trp Gly Trp Asn Asp Ile Ser Cys Ser Leu Lys Gln Lys Ser Val	
215 220 225 230	
tgt cag atg aag aaa ata aac tta tgaatcactc attcttcatg ggcattcgat	1022
Cys Gln Met Lys Lys Ile Asn Leu	
235	
tcattgttat ccaaccatta cacagacacc tgggaaattc tacaggttca cagaatttaa	1082
gtgggcagca aatgggttatg catacactgg cccacatata tccttgtgca tttaccacc	1142
tactctgtca taaaatgaac tttcattgag aattttctat ataccacaga gtatacagag	1202
tccttatgg acacacatgg aactttttgc catcttgttt actcatgccca ttgtatgata	1262
ggttctcttg acctatctgt ttctgtttct ctgttgtttt tttaatgtct ttggatttat	1322
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 <223> poly-A addition motif

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Asn Ser Leu His Thr Tyr Ser Glu Ser Pro Ala Ala Pro Arg Glu Lys
 20 25 30

Pro Ile Arg Asp Leu Arg Lys Pro Gly Ser Pro Ser Leu Leu Leu Thr
 35 40 45

Ser Leu Met Leu Leu Leu Leu Leu Ala Ile Thr Phe Leu Val Ala
 50 55 60

Phe Ile Ile Tyr Phe Gln Lys Tyr Ser Gln Leu Leu Glu Glu Lys Lys
 65 70 75 80

Ala Ala Lys Asn Ile Met His Asn Glu Leu Asn Cys Thr Lys Ser Val
 85 90 95

Ser Pro Met Glu Asp Lys Val Trp Ser Cys Cys Pro Lys Asp Trp Arg
 100 105 110

Leu Phe Gly Ser His Cys Tyr Leu Val Pro Thr Val Ser Ser Ser Ala
 115 120 125

Ser Trp Asn Lys Ser Glu Glu Asn Cys Ser Arg Met Gly Ala His Leu
 130 135 140

Val Val Ile Gln Ser Gln Glu Glu Gln Asp Phe Ile Thr Gly Ile Leu
 145 150 155 160

Asp Thr His Ala Ala Tyr Phe Ile Gly Leu Trp Asp Thr Gly His Arg
 165 170 175

Gln Trp Gln Trp Val Asp Gln Thr Pro Tyr Glu Glu Ser Ile Thr Phe
 180 185 190

Trp His Asn Gly Glu Pro Ser Ser Gly Asn Glu Lys Cys Ala Thr Ile
 195 200 205

Ile Tyr Arg Trp Lys Thr Gly Trp Gly Trp Asn Asp Ile Ser Cys Ser
 210 215 220

Leu Lys Gln Lys Ser Val Cys Gln Met Lys Lys Ile Asn Leu
 225 230 235

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ctg aag aac gcc cac ctg gtg gtc atc aac tcc agg gag gag cag aat	821
Leu Lys Asn Ala His Leu Val Val Ile Asn Ser Arg Glu Glu Gln Asn	
170 175 180	
ttt gtc cag aaa tat cta ggc tcc gca tac acc tgg atg ggc ctc agt	869
Phe Val Gln Lys Tyr Leu Gly Ser Ala Tyr Thr Trp Met Gly Leu Ser	
185 190 195	
gac cct gaa gga gcc tgg aag tgg gtg gat gga aca gac tat gcg acc	917
Asp Pro Glu Gly Ala Trp Lys Trp Val Asp Gly Thr Asp Tyr Ala Thr	
200 205 210 215	
ggc ttc cag aac tgg aag cca ggc cag cca gac gac tgg cag ggg cac	965
Gly Phe Gln Asn Trp Lys Pro Gly Gln Pro Asp Asp Trp Gln Gly His	
220 225 230	
ggg ctg ggt gga ggc gag gac tgt gct cac ttc cat cca gac ggc agg	1013
Gly Leu Gly Gly Gly Glu Asp Cys Ala His Phe His Pro Asp Gly Arg	
235 240 245	
tgg aat gac gac gtc tgc cag agg ccc tac cac tgg gtc tgc gag gct	1061
Trp Asn Asp Asp Val Cys Gln Arg Pro Tyr His Trp Val Cys Glu Ala	
250 255 260	
ggc ctg ggt cag acc agc cag gag agt cac tgagctgcct ttggtgggac	1111
Gly Leu Gly Gln Thr Ser Gln Glu Ser His	
265 270	
cacccggcca cagaaatggc ggtgggagga ggactcttct cacgacctcc tcgcaagacc	1171
gctctgggag agaaataagc actgggagat tggaagcact gctaacattt tgaatttttt	1231
tctctttaat tttaaaaaga tggatatagt ttcttaagct tttatttttt ttccaacttt	1291
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taaaaaaaaa aaaaaaaaaa	1370

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Met Thr Arg Thr Tyr Glu Asn Phe Gln Tyr Leu Glu Asn Lys Val Lys
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Val Gln Gly Phe Lys Asn Gly Pro Leu Pro Leu Gln Ser Leu Leu Leu
20 25 30

Leu Val Ile Ile Cys Val Val Gly Phe Gln Asn Ser Lys Phe Gln Arg
 35 40 45

Asp Leu Val Thr Leu Arg Thr Asp Phe Ser Asn Phe Thr Ser Asn Thr
 50 55 60

Val Ala Glu Ile Gln Ala Leu Thr Ser Gln Gly Ser Ser Leu Glu Glu
 65 70 75 80

Thr Ile Ala Ser Leu Lys Ala Glu Val Glu Gly Phe Lys Gln Glu Arg
 85 90 95

Gln Ala Val His Ser Glu Met Leu Leu Arg Val Gln Gln Leu Val Gln
 100 105 110

Asp Leu Lys Lys Leu Thr Cys Gln Val Ala Thr Leu Asn Asn Asn Gly
 115 120 125

Glu Glu Ala Ser Thr Glu Gly Thr Cys Cys Pro Val Asn Trp Val Glu
 130 135 140

His Gln Asp Ser Cys Tyr Trp Phe Ser His Ser Gly Met Ser Trp Ala
 145 150 155 160

Glu Ala Glu Lys Tyr Cys Gln Leu Lys Asn Ala His Leu Val Val Ile
 165 170 175

Asn Ser Arg Glu Glu Gln Asn Phe Val Gln Lys Tyr Leu Gly Ser Ala
 180 185 190

Tyr Thr Trp Met Gly Leu Ser Asp Pro Glu Gly Ala Trp Lys Trp Val
 195 200 205

Asp Gly Thr Asp Tyr Ala Thr Gly Phe Gln Asn Trp Lys Pro Gly Gln
 210 215 220

Pro Asp Asp Trp Gln Gly His Gly Leu Gly Gly Gly Glu Asp Cys Ala
 225 230 235 240

His Phe His Pro Asp Gly Arg Trp Asn Asp Asp Val Cys Gln Arg Pro
 245 250 255

Tyr His Trp Val Cys Glu Ala Gly Leu Gly Gln Thr Ser Gln Glu Ser
 260 265 270

His

<210> 11
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 <213> Unknown

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Glu Lys Met Ile Ile Lys Glu Leu Asn Tyr Thr Glu Leu Glu Cys Thr
 1 5 10 15

Lys Trp Ala Ser Leu Leu Glu Asp Lys Val Trp Ser Cys Cys Pro Lys
 20 25 30

Asp Trp Lys Pro Phe Gly Ser Tyr Cys Tyr Phe Thr Ser Thr Asp Leu
 35 40 45

Val Ala Ser Trp Asn Glu Ser Lys Glu Asn Cys Phe His Met Gly Ala
 50 55 60

His Leu Val Val Ile His Ser Gln Glu Glu Gln
 65 70 75

<210> 12
 <211> 292
 <212> PRT
 <213> Unknown

<220>
 <223> mammalian protein (ASGPRm is a macrophage derived ASGPR)

<400> 12

Met Thr Arg Thr Tyr Glu Asn Phe Gln Tyr Leu Glu Asn Lys Val Lys
 1 5 10 15

Val Gln Gly Phe Lys Asn Gly Pro Leu Pro Leu Gln Ser Leu Leu Gln
 20 25 30

Arg Leu Arg Ser Gly Pro Cys His Leu Leu Leu Ser Leu Gly Leu Gly
 35 40 45

Leu Leu Leu Leu Val Ile Ile Cys Val Val Gly Phe Gln Asn Ser Lys
 50 55 60

Phe Gln Arg Asp Leu Val Thr Leu Arg Thr Asp Phe Ser Asn Phe Thr
 65 70 75 80

Ser Asn Thr Val Ala Glu Ile Gln Ala Leu Thr Ser Gln Gly Ser Ser
 85 90 95

Leu Glu Glu Thr Ile Ala Ser Leu Lys Ala Glu Val Glu Gly Phe Lys
 100 105 110

Gln Glu Arg Gln Ala Val His Ser Glu Met Leu Leu Arg Val Gln Gln
 115 120 125

Leu Val Gln Asp Leu Lys Lys Leu Thr Cys Gln Val Ala Thr Leu Asn
 130 135 140

Asn Asn Gly Glu Glu Ala Ser Thr Glu Gly Thr Cys Cys Pro Val Asn
 145 150 155 160

Trp Val Glu His Gln Asp Ser Cys Tyr Trp Phe Ser His Ser Gly Met
 165 170 175

Ser Trp Ala Glu Ala Glu Lys Tyr Cys Gln Leu Lys Asn Ala His Leu
 180 185 190

Val Val Ile Asn Ser Arg Glu Glu Gln Asn Phe Val Gln Lys Tyr Leu
 195 200 205

Gly Ser Ala Tyr Thr Trp Met Gly Leu Ser Asp Pro Glu Gly Ala Trp
 210 215 220

Lys Trp Val Asp Gly Thr Asp Tyr Ala Thr Gly Phe Gln Asn Trp Lys
 225 230 235 240

Pro Gly Gln Pro Asp Asp Trp Gln Gly His Gly Leu Gly Gly Gly Glu
 245 250 255

Asp Cys Ala His Phe His Pro Asp Gly Arg Trp Asn Asp Asp Val Cys
 260 265 270

Gln Arg Pro Tyr His Trp Val Cys Glu Ala Gly Leu Gly Gln Thr Ser
 275 280 285

Gln Glu Ser His
 290

<210> 13
 <211> 289
 <212> PRT
 <213> Unknown

<220>
 <223> mammalian protein (DCMP2 short form)

<400> 13

Met Thr Arg Thr Tyr Glu Asn Phe Gln Tyr Leu Glu Asn Lys Val Lys
 1 5 10 15

Val Gln Gly Phe Lys Asn Gly Pro Leu Pro Leu Gln Ser Leu Leu Gln
 20 25 30

Arg Leu Arg Ser Gly Pro Cys His Leu Leu Leu Ser Leu Gly Leu Gly
 35 40 45

Leu Leu Leu Leu Val Ile Ile Cys Val Val Gly Phe Gln Asn Ser Lys
 50 55 60

Phe Gln Arg Asp Leu Val Thr Leu Arg Thr Asp Phe Ser Asn Phe Thr
 65 70 75 80

Ser Asn Thr Val Ala Glu Ile Gln Ala Leu Thr Ser Gln Gly Ser Ser
 85 90 95

Leu Glu Glu Thr Ile Ala Ser Leu Lys Ala Glu Val Glu Gly Phe Lys
 100 105 110

Gln Glu Arg Gln Ala Val His Ser Glu Met Leu Leu Arg Val Gln Gln
 115 120 125

Leu Val Gln Asp Leu Lys Lys Leu Thr Cys Gln Val Ala Thr Leu Asn
 130 135 140

Asn Asn Ala Ser Thr Glu Gly Thr Cys Cys Pro Val Asn Trp Val Glu
 145 150 155 160

His Gln Asp Ser Cys Tyr Trp Phe Ser His Ser Gly Met Ser Trp Ala
 165 170 175

Glu Ala Glu Lys Tyr Cys Gln Leu Lys Asn Ala His Leu Val Val Ile
 180 185 190

20

Asn Ser Arg Glu Glu Gln Asn Phe Val Gln Lys Tyr Leu Gly Ser Ala
195 200 205

Tyr Thr Trp Met Gly Leu Ser Asp Pro Glu Gly Ala Trp Lys Trp Val
210 215 220

Asp Gly Thr Asp Tyr Ala Thr Gly Phe Gln Asn Trp Lys Pro Gly Gln
225 230 235 240

Pro Asp Asn Trp Gln Gly His Gly Leu Gly Gly Gly Glu Asp Cys Ala
245 250 255

His Phe His Pro Asp Gly Arg Trp Asn Asp Asp Val Cys Gln Arg Pro
260 265 270

Tyr His Trp Val Cys Glu Ala Gly Leu Gly Gln Thr Ser Gln Glu Ser
275 280 285

His